

FIGURE 1

FIGURE 2

MVRKKNPPLRNVAESEGEGQILEPIGTEKVSGKNIKEFSADOMSENTDOSDAELNHKEEHSLHVQDPSSSSKKDLKSAVLSEKAGENYE
 SPSKGGNFPPSFPHDEVTDRNMLAFSFPAAGGVCEPLKSPLRSPQRAEADDPQDMACTPSGDSLETKEDQKMSPKATEETGQAQSQANCQGLS
 PVSVASKNPOVPSDGGVRLNKSKTDLLVNDNPDPAPLSPELQDFKCNICGYGYGYGNDPTDLIKHFRKYHLLGLHNRTRODAELDSKILAL
 HNMVQFSHSKDFQKVNRSVFSGVLDINSSRPVLLNGTYDVQVTSGGTFIGIGRKTPDCQGNTKYFRCKFCNFYMGNSSTELEQHFLQ
 THPNKIKASLPSSEVAKPSEKNSNKSIPALQSSDSGDLGKWDQDKITVKAGDDTPVGYSVPIKPLDSSRQNGTEATSYWCKFCFSFSCES
 SSSLKLLEHYGKQHGAIVQSGGLMPELNDKLSRGSVINQNDIPLAKSSEGETMTKTDKSSSGAKKKDFSSKGAEDENMVTSYNCQFCDFRYSK
 SHGPDVIUVGPPLLRYQQLHNIHKCTIKHCPFCPRGLCSPEKHLGEITYPFACRKSNCHCALLLHLSPGAAGGSSRVKHQCHQCSFTT
 PDVDVLLFHYESVHESQASDVVKQEQANHLQGSDDGQQSVKESKEHSCTKCDFITQVEEEISRHYRAHSCYKCRQCSFTAADTQSLLEHFN
 TVHCQEODITTANGEEDGHAISTIKEEPKIDFRVYNLLTPDSKMGEPVSESVKREKLEEKDGKKEKVWTEESSDDLRNVTWRGADILR
 GSPSYTQASLGLLTPVSGTQEQTTLRDSPNVEAAHLARPYGLAVETKGFLOQGAPAGEKEKSGALPQQYPASGENKSKDEQSLLRRR
 GSGVFCANCCLTTKTSLLWRKNANGGYVCNAACGLYQKLHSTPRPLNIIKONNGEQIIRRTRKRNLNEALQAEQLNKQORGNSNEQVNNGSP
 LERRSEDHILTHOREIPLPLSLSKYEAQGSILTKSHTSAQQPVLVSQTLDIHKRMQPLHIOQIKSPQUESTGDPGNSSVSEGKGSSERGSP
 EKYMRPAKHPNNSPPGSPPIEKYQYPLFGLPFVHNDFOSEADWLRFWSKYKLSVPGNPHYLSHVPGLPNPQCQNYVPPYPTFNLPPHFSAVG
 SDNDIPLDLAIKHSRPGPTANGASKEKTYAPPNVVKNEGPLNVVKTEKVDRSTQDELSTKCVHCGIVFLDEVMYALHMSCHGDSGPFOCS
 ICOHLICTDKYDFTTHIQORGLHRMNAQEVINGKPKE

FIGURE 3A

FIGURE 3A

FIGURE 3A

881 original BCY1 (878) CTTCGCCAAGGCCCCCTGGGCCCCGGCAACCGCTCCGGGACTTCCGGGAGCCGAGCTGGCGGGACTCCGGGAGCTGGCGGTCCRG
MC50A19 BCY I (881) CTTCCGCCAAGGCCCCGGCTGGGCCCCGGCAACCGCTCCGGGACTTCCGGGAGCCGAGCTGGCGGGACTCCGGGAGCTGGCGGTCCRG
MC50A6 BCY I (881) CTTCCGCCAAGGCCCCGGCTGGGCCCCGGCAACCGCTCCGGGACTTCCGGGAGCCGAGCTGGCGGGACTCCGGGAGCTGGCGGTCCRG
MC50A8 BCY I (881) CTTCCGCCAAGGCCCCGGCTGGGCCCCGGCAACCGCTCCGGGACTTCCGGGAGCCGAGCTGGCGGGACTCCGGGAGCTGGCGGTCCRG
MC54 .21 BCY I (881) CTTCCGCCAAGGCCCCGGCTGGGCCCCGGCAACCGCTCCGGGACTTCCGGGAGCCGAGCTGGCGGGACTCCGGGAGCTGGCGGTCCRG
MC55 .29 BCY I (881) CTTCCGCCAAGGCCCCGGCTGGGCCCCGGCAACCGCTCCGGGACTTCCGGGAGCCGAGCTGGCGGGACTCCGGGAGCTGGCGGTCCRG
MC55 .32 BCY I (881) CTTCCGCCAAGGCCCCGGCTGGGCCCCGGCAACCGCTCCGGGACTTCCGGGAGCCGAGCTGGCGGGACTCCGGGAGCTGGCGGTCCRG
Consensus (881) CTTCCGCCAAGGCCCCGGCTGGGCCCCGGCAACCGCTCCGGGACTTCCGGGAGCCGAGCTGGCGGGACTCCGGGAGCTGGCGGTCCRG
991 original BCY1 (988) GGCTTCTCTAAACTCTGGTGGGGGGGGCTGGGAAGGGAAAGTGAACTGGCCCTTGTGCCCCTGGGACA
MC50A19 BCY I (991) GGCTTCTCTAAACTCTGGTGGGGGGGGCTGGGAAGGGAAAGTGAACTGGCCCTTGTGCCCCTGGGACA
MC50A6 BCY I (991) GGCTTCTCTAAACTCTGGTGGGGGGGGCTGGGAAGGGAAAGTGAACTGGCCCTTGTGCCCCTGGGACA
MC50A8 BCY I (991) GGCTTCTCTAAACTCTGGTGGGGGGGGCTGGGAAGGGAAAGTGAACTGGCCCTTGTGCCCCTGGGACA
MC54 .21 BCY I (991) GGCTTCTCTAAACTCTGGTGGGGGGGGCTGGGAAGGGAAAGTGAACTGGCCCTTGTGCCCCTGGGACA
MC55 .29 BCY I (991) GGCTTCTCTAAACTCTGGTGGGGGGGGCTGGGAAGGGAAAGTGAACTGGCCCTTGTGCCCCTGGGACA
MC55 .32 BCY I (991) GGCTTCTCTAAACTCTGGTGGGGGGGGCTGGGAAGGGAAAGTGAACTGGCCCTTGTGCCCCTGGGACA
Consensus (991) GGCTTCTCTAAACTCTGGTGGGGGGGGCTGGGAAGGGAAAGTGAACTGGCCCTTGTGCCCCTGGGACA
1101 original BCY1 (1098) CAACCTGTTCTCATGGAGTGTGCAGTACGCATCTGGAGAGGAAGGTGTCCGGCAGACTACAGCCAGGCATCCGAATATTCTCTAA----
MC50A19 BCY I (1098) CAACCTGTTCTCATGGAGTGTGCAGTACGCATCTGGAGAGGAAGGTGTCCGGCAGACTACAGCCAGGCATCCGAATATTCTCTAA----
MC50A6 BCY I (1098) CAACCTGTTCTCATGGAGTGTGCAGTACGCATCTGGAGAGGAAGGTGTCCGGCAGACTACAGCCAGGCATCCGAATATTCTCTAA----
MC50A8 BCY I (1098) CAACCTGTTCTCATGGAGTGTGCAGTACGCATCTGGAGAGGAAGGTGTCCGGCAGACTACAGCCAGGCATCCGAATATTCTCTAA----
MC54 .21 BCY I (1098) CAACCTGTTCTCATGGAGTGTGCAGTACGCATCTGGAGAGGAAGGTGTCCGGCAGACTACAGCCAGGCATCCGAATATTCTCTAA----
MC55 .29 BCY I (1098) CAACCTGTTCTCATGGAGTGTGCAGTACGCATCTGGAGAGGAAGGTGTCCGGCAGACTACAGCCAGGCATCCGAATATTCTCTAA----
MC55 .32 BCY I (1098) CAACCTGTTCTCATGGAGTGTGCAGTACGCATCTGGAGAGGAAGGTGTCCGGCAGACTACAGCCAGGCATCCGAATATTCTCTAA----
Consensus (1101) CAACCTGTTCTCATGGAGTGTGCAGTACGCATCTGGAGAGGAAGGTGTCCGGCAGACTACAGCCAGGCATCCGAATATTCTCTAA----
1211 original BCY1 (1204) ----
MC50A19 BCY I (1208) CCACTAGTCCTGAGTGGGAGATTCTGCAGATAATCA----
MC50A6 BCY I (1208) CCACTAGTCCTGAGTGGGAGATTCTGCAGATAATCA----
MC50A8 BCY I (1208) CCACTAGTCCTGAGTGGGAGATTCTGCAGATAATCA----
MC54 .21 BCY I (1204) ----
MC55 .29 BCY I (1204) ----
MC55 .32 BCY I (1204) ----
Consensus (1211) CAACCTGTTCTCATGGAGTGTGCAGTACGCATCTGGAGAGGAAGGTGTCCGGCAGACTACAGCCAGGCATCCGAATATTCTCTAA----
1248

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FIGURE 3B

MAELRLKGSS NTTECVPPVPT SEHVAEIVGR QGCKIKALRA KTNTYI1KTPV RGEEPVFMVT GRVEDVATZAR REIISAAEHF SMIRASRNKS
GAAFGVAPAL PGQVTIRVRV PYRVVGLVVG PKGATIKRIQ QQTNTYI1ITP SRDRDPVFEI TGAPGNVERA REEIEETHIAV RTGKILEYNN
ENDFLAGSPD AIDSRYSDA WRVHQPGCKP LSTFRQNSLG CIGECGVDSG FEAPRILGEQG GDFGYGGYL F PGYGVGKQDV YYGVAEATSPP
LWAGQENATP TSVLFSSASS SSSSSAKARA GPPGAHRSPA TSAGPELAGI PRRDPGEPLQ GPSKLGGGGL RSPGGGRDCM VCFESEVTA
LVPCGHNLFC MECAVRICER TDPECPVCHI TAAQAIRIFS
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